

015389-003110US

mTRT cDNA clone

- 3496 base pairs

-cDNA: nucleotides 10 to 3435

-ORF: nucleotides 39 to 3404

FIGURE 1

page 1 of 3

GAATTCCGGG	TGGGAGGCC	ATCCCGGCCT	TGAGCACAAT	GACCCGGGCT	50
CCTCGTTGCC	CCGCGGTGCG	CTCTCTGCTG	CGCAGCCGAT	ACCGGGAGGT	100
GTGGCCGCTG	GCAACCTTTG	TGCGGCGCCT	GGGCCCGGAG	GGCAGGCGGC	150
TTGTGCAACC	CGGGACCCCG	AAGATCTACC	GCACTTTGGT	TGCCCAATGC	200
CTAGTGTGCA	TGCACTGGGG	CTCACAGCCT	CCACCTGCCG	ACCTTTCCTT	250
CCACCAGGTG	TCATCCCTGA	AAGAGCTGGT	GGCCAGGGTT	GTGCAGAGAC	300
TCTGCGAGCG	CAACGAGAGA	AACGTGCTGG	CTTTTGGCTT	TGAGCTGCTT	350
AACGAGGCCA	GAGGCGGGCC	TCCCATGGCC	TTCAC TAGTA	GCGTGCGTAG	400
CTACTTGCCC	AACACTGTTA	TTGAGACCCCT	GCGTGTCAGT	GGTGCATGGA	450
TGCTACTGTT	GAGCCGAGTG	GGCGACGACC	TGCTGGTCTA	CCTGCTGGCA	500
CAC TGTGCTC	TTTATCTTCT	GGTGCCCCCC	AGCTGTGCCT	ACCAGGTGTG	550
TGGGTCTCCC	CTGTACC AAA	TTTGTGCCAC	CACGGATATC	TGGCCCTCTG	600
TGTC CGCTAG	TTACAGGCC	ACCCGACCCG	TGGGCAGGAA	TTTCACTAAC	650
CTTAGGTTCT	TACAACAGAT	CAAGAGCAGT	AGTCGCCAGG	AAGCACCGAA	700
ACCCCTGGCC	TTGCCATCTC	GAGGTACAAA	GAGGCATCTG	AGTCTCACCA	750
GTACAAGTGT	GCCTTCAGCT	AAGAAGGCCA	GATGCTATCC	TGTCCCAGAG	800
GTGAGGAGG	GACCCACACAG	GCAGGTGCTA	CCAACCCCAT	CAGGC AAA TC	850
ATGGGTGCCA	AGTCCTGCTC	GGTCCCCCGA	GGTGCC TACT	GCAGAGAAAG	900
ATTTGTCTTC	TAAAGGAAAG	GTGTCTGACC	TGAGTCTCTC	TGGGTCGGTG	950
TGCTGTAAAC	ACAAGCCCCAG	CTCCACATCT	CTGCTGTAC	CACCCCGCCA	1000
AAATGCCCTT	CAGCTCAGGC	CATTATTGA	GACCAGACAT	TTCCCTTACT	1050
CCAGGGGAGA	TGGCCAAAGAG	CGTCTAAACC	CCTCATTCCT	ACTCAGCAAC	1100
CTCCAGCCTA	ACTTGACTGG	GGCCAGGAGA	CTGGTGGAGA	TCATCTTCT	1150
GGGCTCAAGG	CCTAGGACAT	CAGGACCACT	CTGCAGGACA	CACCGTCTAT	1200

FIGURE 1

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mTRL cDNA clone

- 3496 base pairs

-cDNA: nucleotides 10 to 3435

-ORF: nucleotides 39 to 3404

CGCGTCGATA	CTGGCAGATG	CGGCCCCCTGT	TCCAACAGCT	GCTGGTGAAC	1250
CATGCAGAGT	GCCAAATATGT	CAGACTCCTC	AGGTCACATT	GCAGGTTTCG	1300
AACAGCAAAC	CAACAGGTGA	CAGATGCCTT	GAACACACAGC	CCACCGCACCC	1350
TCATGGATT	GCTCCGCCCTG	CACAGCAGTC	CCTGGCAGGT	ATATGGTTT	1400
CTTCGGGCCCT	GTCTCTGCAA	GGTGGTGCT	GCTAGTCTCT	GGGGTACCAG	1450
GCACAATGAG	CGCCGCTTCT	TTAAGAACTT	AAAGAACTTC	ATCTCGTTGG	1500
GGAAATACGG	CAAGCTATCA	CTGCAGGAAC	TGATGTGGAA	GATGAAAGTA	1550
GAGGATTGCC	ACTGGCTCCG	CAGCAGCCCG	GGGAAGGACC	GTGTCCCCGC	1600
TGCAGAGCAC	CGTCTGAGGG	AGAGGATCCT	GGCTACGTTT	CTGTTCTGGC	1650
TGATGGACAC	ATACGTGGTA	CAGCTGCCTA	GGTCATTCTT	TTACATCACA	1700
GAGAGCACAT	TCCAGAAGAA	CAGGCTCTTC	TTCTACCGTA	AGAGTGTGTG	1750
GAGCAAGCTG	CAGAGCATTG	GAGTCAGGCA	ACACCTTGAG	AGAGTGCAGC	1800
TACGGGAGCT	GTCACAAGAG	GAGGTCAGGC	ATCACCAAGGA	CACCTGGCTA	1850
GCCATGCCCA	TCTGCAGACT	GCGCTTCATC	CCCAAGCCCA	ACGGCCTGCG	1900
GCCCATTTGT	AACATGAGTT	ATAGCATGGG	TACCAGAGCT	TTGGGCAGAA	1950
GGAAGCAGGC	CCAGCATTTT	ACCCAGCGTC	TCAAGACTCT	CTTCAGCATG	2000
CTCAACTATG	AGCGGACAAA	ACATCCTCAC	CTTATGGGGT	CTTCTGTACT	2050
GGGTAATGAAT	GACATCTACA	GGACCTGGCG	GGCCTTTGTG	CTGCGTGTGC	2100
GTGCTCTGGA	CCAGACACCC	AGGATGTACT	TTGTTAAGGC	AGATGTGACC	2150
GGGGCCTATG	ATGCCATCCC	CCAGGGTAAG	CTGGTGGAGG	TTGTTGCCAA	2200
TATGATCAGG	CACTCGGAGA	GCACGTACTG	TATCCGCCAG	TATGCAAGTG	2250
TCCGGAGAGA	TAGCCCAAGGC	CAAGTCCACA	AGTCCTTTAG	GAGACAGGTC	2300
ACCACCCCTCT	CTGACCTCCA	GCCATACATG	GGCCAGTTCC	TTAAGCATCT	2350
GCAGGATTCA	GATGCCAGTG	CACTGAGGAA	CTCCGTTGTC	ATCGAGCAGA	2400

FIGURE 1

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mTfL cDNA clone

- 3496 base pairs

-cDNA: nucleotides 10 to 3435

-ORF: nucleotides 39 to 3404

GCATCTCTAT	GAATGAGAGC	AGCAGCAGCC	TGTTTGACTT	CTTCCTGCAC	2450
TTCCCTGCGTC	ACAGTGTCGT	AAAGATTGGT	GACAGGTGCT	ATACGCAGTG	2500
CCAGGGCATC	CCCCAGGGCT	CCAGCCTATC	CACCCCTGCTC	TGCAGTCTGT	2550
GTTTCGGAGA	CATGGAGAAC	AAGCTGTTTG	CTGAGGTGCA	GCGGATGGG	2600
TTGCTTTTAC	GTTTGTGTTGA	TGACTTTCCTG	TTGGTGACGC	CTCACTTGA	2650
CCAAAGCAAAA	ACCTTCCCTCA	GCACCCCTGGT	CCATGGCGTT	CCTGAGTATG	2700
GGTGCAATGAT	AAACTTGCAG	AAGACAGTGG	TGAACCTTCCC	TGTGGAGCCT	2750
GGTACCCCTGG	GTGGTGCAGC	TCCATACCCAG	CTGCCCTGCTC	ACTGCCCTGTT	2800
TCCCTGGTGT	GGCTTGCTGC	TGGACACTCA	GACTTTGGAG	GTGTTCTGTG	2850
ACTACTCAGG	TTATGCCCCAG	ACCTCAATTA	AGACGAGCCT	CACCTTCCAG	2900
AGTGTCTTCA	AAGCTGGGAA	GACCATGCGG	AACAAGCTCC	TGTCGGTCTT	2950
GCGGTTGAAG	TGTCACGGTC	TATTTCTAGA	CTTGCAGGTG	AACAGCCTCC	3000
AGACAGTCTG	CATCAATATA	TACAAGATCT	TCCTGCTTCA	GGCCTACAGG	3050
TTCCATGTCAT	GTGTGATTCA	GCTTCCCCTT	GACCAGCGTG	TTAGGAAGAA	3100
CCTCACATTC	TTTCTGGGCA	TCATCTCCAG	CCAAGCATCC	TGCTGCTATG	3150
CTATCCTGAA	GGTCAAGAAAT	CCAGGAATGA	CACATAAAGGC	CTCTGGCTCC	3200
TTTCCTCCTG	AAGCCGCACA	TTGGCTCTGC	TACCAGGCCT	TCCTGCTCAA	3250
GCTGGCTGCT	CATTCTGTCA	TCTACAAATG	TCTCCTGGGA	CCTCTGAGGA	3300
CAGCCCAAAA	ACTGCTGTGC	CGGAAGCTCC	CAGAGGCGAC	AATGACCATC	3350
CTTAAAGCTG	CAGCTGACCC	AGCCCTAAGC	ACAGACTTTC	AGACCATTTT	3400
GGACTAACCC	TGTCCTCCTC	CGCTAGATGA	ACATGAAGGG	CGAATTCCAG	3450
CACACTGGCG	GCCGTTACTA	GTGGATCCGA	GCTCGGTACC		3496
			AAGCTT		

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FIGURE 2

1122 Amino Acids
127,979 kD
pI ~ 10.4

MTRAPRCPAV RSLRLSRYRE VWPLATFVRR LGPEGRRLVQ PGDPKIYRTL VAQCLVCMHW GSQPPADLS FHQVSSLKEL 80
VARVVQRLCE RNERNVLAFG FELLNEARGG PPMAFTSSVR SYLPNTVIET LRVSGAWMLL LSRVGGDLLV YLLAHCALYL 160
LVPPSCAYQV CGSPLYQICA TTDIWPVSVA SYRTPRPVGR NFTNLRFLQQ IKSSRQEAP KPLALPSRGT KRHLSTSTS 240
VPSAKKARCYPVPRVEEGPH RQVLPTPSGK SWVSPARSP EVPTAEKDLS SKGKVSDLSL SGSVCCCKHKP SSTSLSPPR 320
QNAFQLRPFIE TRHFLYSRG DGQERLNPSF LLSNLQPNLT GARRLVEIIF LGSRPRTSGP LCRTHRLSRR YWQMRPLFQQ 400
LLVNHAEQYVRLLRSHCRF RTANQQVTDALNTSPPHLMD LLRLHSSPWQ VYGFRLRACLK KVVASASLWGT RHNERRRFFKN 480
LKKFISLGKY GKLSLQELMW KMKVEDCHWL RSSPGKDRVP AAHRLRERI LATFLFWLMD TYVVQLLRSF FYITESTFQK 560
NRLFFYRKSV WSKLQSIGVR QHLERVRLRE LSQEEVRHHQ DTWLAMPICR LRFIPKPNGL RPVNMMSYSM GTRALGRRKQ 640
AQHFTQRLKT LFSMLNYERT KHPHLMGSSV LGMNDIYRTW RAFVLRVRAL DQTPRMFYVK ADVTGAYDAI PQGKLVEVVA 720
NMIRHSESTY CIRQYAVVRR DSQGVHKSFRQVTTLSL QPYMGQFLKH LQSDASALR NSVIEQSI MNESSSLFD 800
FELHFLRHSV VKIGDRCYTQ CQIPQGGSL STLLCSLCFG DMENKLFAEV QRDGLLRFV DDFLLVTPHL DQAKTFLSTL 880
VHGVPEYGCM INLQKTVNF PVEPGTLGGA APYQLPAHCL FPWCGLLLDT QTLEVFCDYS GYAQTSIKTS LTFQSVFKAG 960
KTMRNKLLSV LRLKCHGLFL DLQVNSLQTV CINIYKIFLL QAYRFHACVI QLPFDQVRK NLTFFLGHS SQASCCYAIL 1040
KVKNPGMTLK ASGSFPPEAA HWLCYQAFLL KLAHHSVIYK CLLGPLRTAQ KLLCRKLPEA TMTILKAAAD PALSTDFQTI 1120
LD 1122

H:\CLIENT\GERON\003110US\FIGURE_2.SEQ

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FIGURE 3

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mTRT vs. hTRT amino acid alignment

mTRT MTRAPRCPAVRSLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHWGSQPPADLSFHQVS
hTRT MPRAPRCRAVRSLRSRYREVWPLATFVRRLGPEGRRLVQPGDPAAFRALVAQCLVCVPWDARPPPAAPSRQVS

SLKELVARVVQRLCERNERNVLAFGFELLNEARGPPMAFTSSVRSYLPNTVIETLRVSGAWMLL SRVGDDLLV
 CLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPEAFTTSVRSYLPNTVTDALRGSAWGLLRRVGGDDVLV .

YLLAHCALYLLVPPSCAYQVCGSPLYQICATTDIWPSVSASYRTPRVGRNFTNRLFLQIKSSSRQEAQPKPLAL
 HLLARCALFVLVAPSCAYQVCGPPLYQLGAATQARPPPHAS.GPRRRLLG CERAWNHSVREAGVPLGL

PSRGTKRHLSTSTSVPSAKKARCYPVPRVEEGPHRQVLPTPSGKSWVSPARSPEVP...TAEKDLSSKGKVS
 PAPGARRRGGASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAAEEATSLEGALSG

LSLS.GSVCCCKHKPSSSTLSLSPPRQNAFQLRP.FIETRHFLYSRGDQGERLNPSFLLSNLQPN LTGARRLVEIF
 TRHSHPSVGRQHHAAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGD.KEQLRPSFLLSSLRPSLTGARRLVETIF

LGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQYVRLLRSHCRFRTA..... NQQVTDA
 LGSRPWMPGTPRRLRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPGQSVAAPEE

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FIGURE 3

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mTRT vs. hTRT amino acid alignment

LNTSPPHLMDLLRLHSSPWQVYGFLRACLCKVVSASLWGTRHNERFFKNLKKFISLGKYGKLSLQELMWKMKVE
EDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGSRHNERFLRNTKKFISLGKHAKLSLQELTWKMSVR

Motif T

DCHWLRSPPGKDRVPAAEHRLRERILATFLFWLMDTYVVQLRSFFYITESTFQKNRLLFFYRKSVWSKLQSIGVR
DCAWLRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVVELLRSSFFYVTETTFQKNRLLFFYRKSVWSKLQSIGIR

Motif 1.

Motif 2

QHLERVRLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPVNMMDYVVVGARTFRREKRAERLTSRVKALFSVL
QHLKR

Motif A

NYERTKHPHLMGSSVLGMNDIYRTWRAFLRVLRVRAALDQTPRMVFKADVTGAYDAIPQGKLVEVVANMIRHSESTY
NYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIAIIK.PQNTY

CIRQYAVVRRDSQQGVHKSFRRQVTTLSDLQPYMGQFLKHLQSDASALRNSVVEQSISSMNESSSLFDFFLHF
CVRRYAVVQKAAHGHVVRKAFKSHVSTLTDLQPYMRQFVAHLQET..SPLRDAVVIEQSSSLNEASSGLFDVFLRF

Motif B'

Motif C

Motif D

LRHSVVKIGDRCYTQCQIPQGSSSLSTLLCSLCFGDMENKLF AEVQRDGLLLRFVDDFLLVTPHLDQAKTFLSTL
MCHHAVRIGKSYVQCQIPQGSSILSTLLCSLCYGD MENKLFAGIRRDGLLRLVDDFLLVTPHLTHAKTFLRTL.

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FIGURE 3

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mTRT vs. hTRT amino acid alignment

Motif D	Motif E
VHGVPEYGC MIN LQKTVVNFPVEPGTLGGAAPYQLPAHCLFPWCGLLLDQTLEVFCDYSGYAQTSIKTSLTFQS	
VRGVPEYGC VVN LRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNR	
VFKAGKTMRNKLLSVLRKCHGLFLDLQVNSLQTVCTNIYKIFLLQAYRFHACVQLPFDQVRKNTFFLGIIS	
GFKAGRNMRRKLFGLVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVQLPFFHQVWKNPTFFLRVIS	
SQASCCYAILKVKNPMTLKASGS...FPPEAAHWLCYQAFLLKLAHSHVYKCLLGPLRTAQKLLCRKLPEATM	
DTASLCYSILKAKNAGMSLGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQQLSRKLPGTTL	
TILKAAADPALSTDFQTILD 1122	
TALEAAANPALPSDFKTILD 1132	

FIGURE 4

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		Motif T											
		WL	V	LL	FFY	TE	R	YY	RK	W	L	I	
TRT con		WL	MSVYVVELLR	SFFYV	TETTFQ	KNR	LF	FFYR	KS	V	WSK	LQ	
hTRT/hEST2p		WL	MSVYVVELLR	SFFYV	TETTFQ	KNR	LF	FFYR	KS	V	WSK	LQ	
mTRT		WL	MDTYV	VQ	LLR	SFFY	ITE	STFQ	KNR	LF	FFYR	KS	
Ea_p123		W	FEDL	V	SL	R	CF	FV	TE	Q	K	S	
Sc_EST2p		W	L	FR	Q	L	P	K	I	Q	T	F	
Sp_Trt1p		W	L	Y	N	S	F	I	P	L	Q	S	
		Motif 1						Motif 2					
		LR						IPK					
TRT con		EVRQ						HREAR					
hTRT/hEST2p		EVRH						H					
mTRT		KEVEE						W					
Ea_p123		CRNH						N					
Sc_EST2p		NNVR						M					
Sp_Trt1p		FRLIT						N					
		Motif A						K					
		P						YF					
TRT con		PPPEL						Y					
hTRT/hEST2p		QTPRM						Y					
mTRT		GQPKL						F					
Ea_p123		VLPEL						Y					
Sc_EST2p		FGRKK						Y					
Sp_Trt1p		FRLIT						N					

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FIGURE 4

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	Motif B'					Motif C				
TRT con	K	Y	Q	GIPQ	GSLS	L	Y	D	LLR	DDFLL IT
htr/hEST2p	KSVV	QCQ	GIPQ	GSIL	STLL	CSLC	YCGD	MENKLFAGI	LLRLV	DDFLLVTPHLTH
mTRT	RCYT	QCQ	GIPQ	GSLS	STLL	CSLC	FGDM	MENKLFAGI	LLRFV	DDFLLVTPHLDQ
Ea_p123	KFYK	QTK	GIPQ	GSIL	CVSS	ILSF	YATL	EESSLGFL	LMRLT	DDYLLITTQENN
Sc_EST2p	KCYI	RED	GLF	QGS	SLSA	PIVDL	VYDD	LLEFYSEFK	ILKL	ADDFLIISTDQQQ
Sp_Trtlp	SQYL	QKV	GIPQ	GSIL	SSFL	CHFYMED	LIDE	YLSFT	LLRV	VDDFLFITVNNKKD
	Motif D					Motif E				
TRT con	A	F	G	N	K	W	G			
htr/hEST2p	AKT	FLR	TLV	RGV	PEYGC	VVNLR	RKTVV	HGLFP	WCGLLL	
mTRT	AKT	FLS	TLV	HGV	PEYGC	MINL	QKTVV	HCLFP	WCGLLL	
Ea_p123	AVL	FIE	KLIN	VSRE	NGFK	FNMK	KLQT	QDYCD	WIGISI	
Sc_EST2p	VINI	KKLAM	G	G	QKYN	AKAN	RDKILA	KELEV	WKHSST	
Sp_Trtlp	AKK	FLN	LSL	R	GFEK	HNFST	SLEKTVI	KKRMP	FFGF	FSV

FIGURE 5
General and Murine Specific TERT Amino Acid Motifs

x_n - any aa

h = A, L, I, V, P, F, W, M

p = G, S, T, Y, C, M, Q

c = D, E, H, K, R.

r_1 = I, L

r_5 = F > L

r_9 = R > K

r_{13} = G > H

r_{17} = T > S

r_2 = R, Q

r_6 = P > F

r_{10} = G > V

r_{14} = C > A

r_3 = Y > F

r_7 = S > L

r_{11} = N > S

r_{15} = I > V

r_4 = K > H

r_8 = L > M

r_{12} = W > F

r_{16} = L > V

">" = 1st aa preferred over the 2nd

gen = general TERT motif

hum = human specific motif

mus = mouse specific motif

bold residues are species specific changes

Motif T

gen W-r₁-x₄-h-h-x-h-h-r₂-p-F-F-Y-x-T-E-x-p-x₃-p-x_{2,3}-r₃-r₃-R-r₄-x₂-W

hum W-r₁-x₄-h-h-x-h-h-r₂-p-F-F-Y-V-T-E-x-p-x₃-p-x_{2,3}-r₃-r₃-R-r₄-x₂-W

mus W-r₁-x₄-h-h-x-h-h-r₂-p-F-F-Y-I-T-E-x-p-x₃-p-x_{2,3}-r₃-r₃-R-r₄-x₂-W

Motif 1

gen h-R-h-r₁-P-K-x₂-p

hum h-R-h-r₁-P-K-x-D-p

mus h-R-h-r₁-P-K-x-N-p

Motif 2

gen r₅-R-h-I-x₂-h

hum "

mus "

Motif A

gen P-c-x-r₃-F-h-x-h-D-h-x₂-r₁₄-Y-D-x-r₁₅

hum P-E-x-r₃-F-h-x-V-D-h-x₂-r₁₄-Y-D-x-r₁₅

mus P-R-x-r₃-F-h-x-D-D-h-x₂-r₁₄-Y-D-x-r₁₅

Motif B'

gen Y-x-r₂-x₂-G-r₁-r₆-Q-G-r₇-x-r₁₆-S-x-h-r₁

hum Y-x-r₂-x₂-G-r₁-r₆-Q-G-r₇-I-r₁₆-S-x-h-r₁

mus Y-x-r₂-x₂-G-r₁-r₆-Q-G-r₇-S-r₁₆-S-x-h-r₁

Motif C

gen r₁-r₈-r₉-h-x-D-D-r₃-L-h-R₁₅-R₁₇

hum r₁-r₈-r₉-L-x-D-D-r₃-L-h-R₁₅-R₁₇

mus r₁-r₈-r₉-F-x-D-D-r₃-L-h-R₁₅-R₁₇

Motif D

gen r₁₀-x₂-C-x-p-x₃-r₁₁-x₂-K-x₃

hum r₁₀-x₂-C-x-p-x₃-r₁₁-R-K-x₃

mus r₁₀-x₂-C-x-p-x₃-r₁₁-Q-K-x₃

Motif E

gen r₁₂-x-r₁₃-x-r₇-x

hum "

hum "

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FIGURE 6
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mTRT Promoter Region
-cDNA start at 1680
-ORF start at 1709

AAAGCAGGCC	TGTAACACAA	AGGTCCTTTT	TCCTGGTTTA	TCGTGGCTGG	50
TAGACAAATT	CCACTTGTTT	TCCACTTCAG	TTTTTTCTAC	TCGGTTGTTA	100
TTGGATTCTG	ATGCTTGAAC	CCAGGTTGGT	AGTCAGCAAG	TGCACCCCTT	150
CCTTCTTTT	CTTGGTTTTT	TTGAGGCAGG	TCTCATTTTG	CCCAAGTGGA	200
CCTAAATTTC	AGCATGTAGT	GGCTGGTTTN	GAATGCTTTT	TCATCCTGCT	250
NTACTTCCCA	AGAGTAGCTA	ACAAAGTGTC	ACCACCAATG	CCCGCGATAT	300
TTTTATTTT	GAGACTGTTT	TCTATGCTGG	TTTCTTTGGG	GAACATACAT	350
AAGGTAGCTT	ACAAAGTGTC	ACCACCATGC	CCCGCGATAT	TCTTATTTT	400
GAGACTGTTT	TCTATGCTGG	TTTCTTTGGG	GAACATACAT	AAGGTAGCTT	450
CATTGTTGGC	ATAAATTCT	CAGTTCAGGC	CCATATCTCT	TAAGTAGCAG	500
AACTAAGCCA	AATCTTCAAA	CAAAACCCCTT	CAAAAAGACT	GATGTCCACT	550
AAACGGACTT	CTAAAATAGC	TCCCTGTAAT	CCTGAGCAIT	TACCAAGGCG	600
GCAGACTTCC	TATAAGGGAG	TAAATATGAA	AACGCGCCTG	TTCAAATGCT	650
AGGTCGGTGG	ATAGAAAGCAA	TTTCCCTCAGA	AAGCTGAAGG	CACCAAAGGT	700
TATATTTGTT	AGCATTTTCAG	TGTTTGCCAA	ACTCAGCTAC	AGTAGAGATC	750
ACAGATTCCC	TATTTCCCAG	AGATTCAAAA	TTCAGCAGCC	CCTCTCTAAC	800
TATGGCTCAG	AGTCGTGTCA	TTACATATGC	CCCAACAACA	ACCCCAACCC	850
CTATCCTACC	CCCGCCTCAC	ACGTGCAAGT	ACTATCACAG	TTGCCAACCT	900
AGCAGAGCTG	CCATCCTAAG	GTCGAGGTGG	CCGCTTTGGC	TGTGTGCACA	950
GGCAAGCGCC	CTCACCCCAAT	GGCCCTGGCC	TTGCTATGGG	TGCGTGAGTT	1000
GAGATGATGC	TCTGGACTCT	GAGGTGAAGG	CCACTGGAAC	AGTGAAAAAA	1050
GCTAACGCAG	GGCTTTTACC	TAGGTCCCCT	TCCTTTGGTG	GTGGGTGTTT	1100
ACGGAACATA	TTTGGGATCT	GGAGTGATG	GTCGCACCAC	AATAAGCCT	1150

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FIGURE 6

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TAACCTATAT	AGTAGAATGT	TCAGCTGTAA	TCATTAAGAA	CTGAGATTGC	1200
CACCACCCAC	CTCACTGTCT	GTGTCAACCA	CAGCAGGCTG	GAGCAGTCAG	1250
CTCAGGAACA	GGCAAAACCT	TAGGTCCTCC	GCCTACCTAA	CCTTCAATAC	1300
ATCAAGGATA	GGCTTCTTTG	CTTGCCCAAA	CCTCGCCCCA	GTCTAGACCA	1350
CCTGGGGATT	CCCAGCTCAG	GGCGAAAGG	AAGCCCCGAGA	AGCATTTCTGT	1400
AGAGGGAAAT	CCTGCATGAG	TGCGCCCCCT	TTCGTTACTC	CAACACATCC	1450
AGCAACCACT	GAACTTGGCC	GGGGAACACA	CCTGGTCCTC	ATGCACCAGC	1500
ATTGTGACCA	TCAACGGAAA	AGTACTATTG	CTGCGACCCC	GCCCCTTCCG	1550
CTACAACGCT	TGGTCCGCCT	GAATCCCCGC	CCTTCCTCCG	TTCCCAGCCT	1600
CATCTTTTC	GTCGTGGACT	CTCAGTGGCC	TGGGTCCTGG	CTGTTTCTA	1650
AGCACACCCCT	TGCATCTTGG	TTCCCCGCACG	TGGGAGGCC	ATCCCGGCCT	1700
TGAGCACAAAT	GACCCGCGCT	CCTCGTTGCC	CCGCGGTGCG	CTCTCTGCTG	1750
CGCAGCCGAT	ACCGGGAGGT	GTGGCCCGCTG	GCAACCTTTG	TGCGGCGCCT	1800
GGGGCCCCG					1808

H:\CLIENT\GERON\003110US\FIGURE_6.SEQ

FIGURE 7
mTERT Genomic DNA

lambda-mTERT (~23 Kbp)

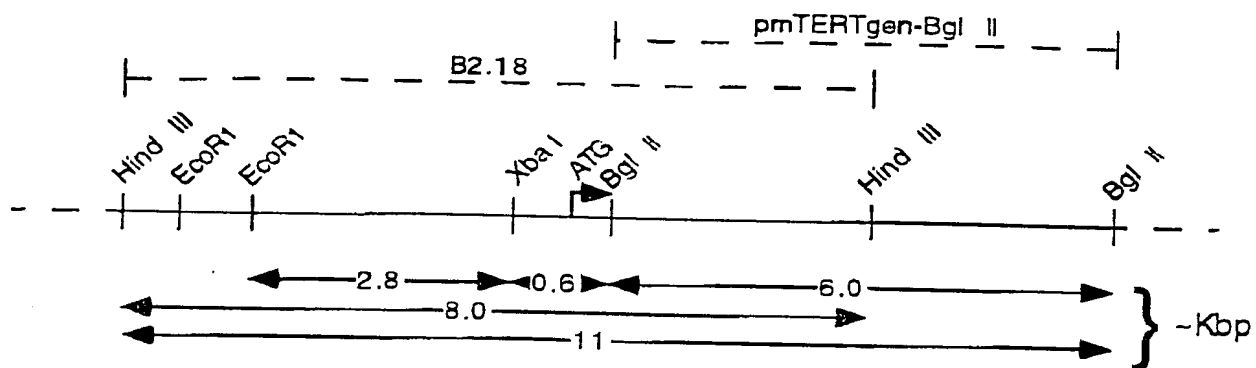


FIGURE 8

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Preliminary sequence of B2.18, containing the promoter region of mTERT.
 cDNA starts at: 2057
 ORF starts at: 2087

AAACAAAGTC	AATGAGGAAT	GGCTGTGTTT	CATCTTGACC	ACTGAGAAAGT	50
AAAACCGGGT	GCAGTGATGT	CCAAAAAGGC	AAGGTGACAG	CAGAGCGGAG	100
GCCCCAATCT	AGAGCAGGGC	CTTCGGTTTG	AATGGGGAG	ATCAAACGGG	150
AGTTGGTTTC	TGCCAGCACG	TTGGGGTAGA	AGGTGGAACA	TGAAAGGTCC	200
CCGAGGATTT	CGAGAGTCCA	TAGGGGTAGC	GACACCCGAG	GTCTTCTTTT	250
TCACCTCCTT	CCCTGCAGGG	GAGATGACTT	TTACCAACAGT	CGTTTATGGG	300
AAAGTTCCCTA	GGGGCAGCCC	CTCCCCAAAA	AGGCTCTCCC	TGGCCTCATG	350
TTTCAAAGCA	CAGCTTTTTA	AAGCAGGCCT	GTTAAGCACAC	AAGGATCCCC	400
AATCCTGGCT	TCATCGTTGG	CTGGTAGACA	ACTTCCACTC	GTTTTCCACT	450
TCAGTTTCTT	CTAACTCTGT	TGTTATTTGA	TTCTGATGCT	TGAACCCAGG	500
GTTGTGTAGT	CAGCAAGTGC	TACCCCTCTC	TCCTCTTCTT	TGTTTTTTTG	550
AGGCAGGTC	TCATTTTGCC	CAAGTGGACC	TAAATTTTCA	CATGTAGCTG	600
GCCTGGTTTT	GAATGCCCTC	TCATCCTGCC	TCTACTTCCC	AAGAGTAGCT	650
TACAAAGTGT	CACCACCATG	CCCCGGGATA	TTCTTATTTT	TGAGACTGTT	700
TTCTATGCTG	GTTTCTTTTG	GGAACCTACAC	TAAGGTAGCT	TACAAGTGTG	750
CACCACCATG	CCCCGGGATA	TTCTTATTTT	TGAGACTGTT	TTCTATGCTG	800
GTTTCTTTTG	GGAACCTACAC	TAAGGTAGCT	TCATTTGTTG	CATAAAATTC	850
TCAGTTCAGG	CCCATATCTC	CTAAGTAGCA	GAACTAAGCA	AATCTCAAAC	900
AAACCCCTCA	AAAAGACTGA	TGTCCTACTAA	ACGGACTTCT	AAAATAGCTC	950
CCTGTAATCC	TGAGCATTTA	CAAGGGGCA	GACCTCCTAT	AAGGGAGTAA	1000
ATATGAAAAC	GCCTGTGTTT	AAATGCTAGG	TCGGTGGATA	GAAGCAATTT	1050
CCTCAGAAAG	CTGAAGGCAC	CAAAGGTTAT	ATTGTTAGC	ATTTTCAAGT	1100
TTGCCAAACT	CAGCTACAGT	AGAGATCACA	GATTCCTTAT	TTCCCAGAGA	1150
TTCAAAATTC	AGCAGCCCCT	CTCTAACTAT	GGCTCAGAGT	CGTGTCTATTA	1200
CATATGCCCC	AACAACAACC	CCACCCCTTA	TCCTACCCCC	GCCTCACACG	1250
TGCAAGTACT	ATCACAGTTG	CCAACCTAGC	AGAGCTGCCA	TCCTAAGGTC	1300
GAGGTCGCCG	CTTTGGCTGT	GTGCACAGGC	AAGCGCCCTC	ACCCAATGGC	1350
CCTGGCCTTG	CTATGGGTGC	GTGAGTTGAG	ATGATGCTCT	GGACTCTGAG	1400

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FIGURE 8

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GTGAAGGCCA CTGGAACAGT GAAAAAAGCT AACGCAGGGC TTTTACCTAG 1450
 GTCCCTTTC TTTGGTGGT GGTGTTTACG GAACATATTT GGGATCTGGA 1500
 GTGTATGGTC GCACCACAAAT AAAGCCTTAA CCTATATAGT AGAATTCAG 1550
 CTGTAATCAT TAAGAACTGA GATTGCCACC ACCCACCTCA CTGTCTGTGT 1600
 CAACCACAGC AGGCTGGAGC AGTCAGCTCA GGAACAGGCA AAACCTTAGG 1650
 TCCCTCCGCC TACCTAACCT TCAATACATC AAGGATAGGC TTTCTTGCTT 1700
 GCCCAAACT CGCCCCAGTC TAGACCACCT GGGGATTCCT AGCTCAGGGC 1750
 GAAAAGGAAG CCCGGAAGC ATTCTGTAGA GGGAAATCCT GCATGAGTGC 1800
 GCCCCCTTC GTTACTCCAA CACATCCAGC AACCACTGAA CTTGGCCGGG 1850
 GAACACACCT GGTCTCTATG CACCAGCATT GTGACCATCA ACGGAAAAGT 1900
 ACTATTGCTG CGACCCCGCC CCTTCCGCTA CAACGCTTGG TCCGCCCTGAA 1950
 TCCCGCCCCT TCCTCCGTTT TTTTCTAAGC ACACCCTTGC ATCTTGTTTC 2000
 AGTGGCCTGG GTCCCTGGCTG CCCGGCCTTG AGCACAATGA CCCGCGCTCC 2050
 CCGCACGTGG GAAGGCCCAT CCGGGCCTTG AGCACAATGA CCCGCGCTCC 2100
 TCGTTGCCCC GCGGTGCGCT CTCTGCTGCG GAGCCGATAC CCGGAGGTGT 2150
 GGCCGCTGGC AACCTTTGTG CGGCGCCTTG GCGCCGAGGG CAGGCGGCTT 2200
 GTGCAACCCG GGGACCGAAG ATCTACCGCA CTTTGGGTTG CCAATGCCT 2250
 AGTGTGCATG CACTGGGGCT CACAGCCTCC ACCTGCCGAC CTTTCTTCC 2300
 ACCAGGTGGG CCTCCAGGCG GGATCCCCAT GGGTCAGGGG CGGAAAGCCG 2350
 GGAGGACGTG GGATAGTGCG TCTAGCTCAT GTGTCAAGAC CCTCTTCTCC 2400
 TTACCAGGTG TCATCCCTGA AAAGAGCTGG TGGCCAGGGT TGTGCAGAGA 2450
 CTCTGCCGAGC GCAACGAGAG AAACGTGCTG GCTTTTGGCT TTGAGCTGCT 2500
 TAACGAAGCC AGAAGCGGGC CTCCCATGGC CTTCACTAAT TAGCGTGCGT 2550
 AAGTACTTG CCCAACACTG TTATTGAAA CTTGCGTGTC AGTGGTGAT 2600
 GGAATGCTACT GTTGAGCCGA ATGGCGACA CTGCTGGTC TACCTGCTGG 2650
 C 2651

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FIGURE 9
mTERT Genomic DNA

pmTERTKO

